
Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: Tue May 22 09:08:03 EDT 2007

Validated By CRFValidator v 1.0.2

Application No: 10574085 Version No: 1.0

Input Set:

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Started: 2007-05-21 11:28:46.134

Finished: 2007-05-21 11:28:46.514

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 380 ms

Total Warnings: 6

Total Errors: 0

No. of SeqIDs Defined: 6

Actual SeqID Count: 6

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<140> 10574085
<141> 2007-05-21
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<151> 2006-03-30
<150> PCT/JP2004/014575
<151> 2004-09-28
<150> JP 2003-340092
<151> 2003-09-30
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<211> 1776
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic DNA coding for a fusion
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                                                                     60
tragcatttg ctgatgttcc trtaactrca trtraatttg ctaaagrgaa atragagaar
                                                                    120
                                                                    180
tttgacaaga aagttattct atctaatcta aataagccgc atgctttgtt atggggacca
gataatcaaa tttggttaac tgagcgagca acaggtaaga ttctaagagt taatccagag
                                                                    240
                                                                    300
tcqqqtaqtq taaaaacaqt ttttcaqqta ccaqaqattq tcaatqatqc tqatqqqcaq
aatggtttat taggttttgc cttccatcct gattttaaaa ataatcctta tatctatatt
                                                                   360
tcaggtacat ttaaaaatcc gaaatctaca gataaagaat taccgaacca aacgattatt
                                                                    420
                                                                    480
cqtcqttata cctataataa atcaacaqat acqctcqaqa aqccaqtcqa tttattaqca
ggattacctt catcaaaaga ccatcagtca ggtcgtcttg tcattgggcc agatcaaaag
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                                                                    660
caagcacaac atacgccaac tcaacaagaa ctgaatggta aagactatca cacctatatg
ggtaaagtac tacgcttaaa tcttgatgga agtattccaa aggataatcc aagttttaac
                                                                    720
ggggtggtta gccatattta tacacttgga catcgtaatc cgcagggctt agcattcact
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ccaaatggta aattattgca gtctgaacaa ggcccaaact ctgacgatga aattaacctc
                                                                    840
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attgtcaaag gtggcaatta tggttggccg aatgtagcag gttataaaga tgatagtggc
                                                                   960
tatgcttatg caaattattc agcagcagcc aataagtcaa ttaaggattt agctcaaaat
                                                                  1020
ggagtaaaag tagccgcagg ggtccctgtg acgaaagaat ctgaatggac tggtaaaaac
tttgtcccac cattaaaaac tttatatacc gttcaagata cctacaacta taacgatcca
                                                                   1080
acttqtqqaq aqatqaccta catttqctqq ccaacaqttq caccqtcatc tqcctatqtc
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tataagggcg gtaaaaaagc aattactggt tgggaaaata cattattggt tccatcttta
                                                                   1200
aaacgtggtg tcattttccg tattaagtta gatccaactt atagcactac ttatgatgac
                                                                   1260
                                                                   1320
gctgtaccga tgtttaagag caacaaccgt tatcgtgatg tgattgcaag tccagatggg
aatgtcttat atgtattaac tgatactgcc ggaaatgtcc aaaaagatga tggctcagta
                                                                   1380
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acaaatacat tagaaaaccc aggatetete attaagttea cetataagge taaggagete
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ggcaaggcca ggatgccgga gttcgtggcc cagcgcaccg gccagttgct gcagggcgtg
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Leu Val Thr Leu Ser Ala Phe Ala Asp Val Pro Leu Thr Pro Ser Gln
                               25
Phe Ala Lys Ala Lys Ser Glu Asn Phe Asp Lys Lys Val Ile Leu Ser
                           40
Asn Leu Asn Lys Pro His Ala Leu Leu Trp Gly Pro Asp Asn Gln Ile
                       55
Trp Leu Thr Glu Arg Ala Thr Gly Lys Ile Leu Arg Val Asn Pro Glu
                   7.0
                                       75
Ser Gly Ser Val Lys Thr Val Phe Gln Val Pro Glu Ile Val Asn Asp
                         90
              8.5
Ala Asp Gly Gln Asn Gly Leu Leu Gly Phe Ala Phe His Pro Asp Phe
                               105
Lys Asn Asn Pro Tyr Ile Tyr Ile Ser Gly Thr Phe Lys Asn Pro Lys
       115
                           120
                                               125
Ser Thr Asp Lys Glu Leu Pro Asn Gln Thr Ile Ile Arg Arg Tyr Thr
                       135
                                           140
Tyr Asn Lys Ser Thr Asp Thr Leu Glu Lys Pro Val Asp Leu Leu Ala
                   150
                                       155
Gly Leu Pro Ser Ser Lys Asp His Gln Ser Gly Arg Leu Val Ile Gly
               165
                                  170
Pro Asp Gln Lys Ile Tyr Tyr Thr Ile Gly Asp Gln Gly Arg Asn Gln
Leu Ala Tyr Leu Phe Leu Pro Asn Gln Ala Gln His Thr Pro Thr Gln
                           200
Gln Glu Leu Asn Gly Lys Asp Tyr His Thr Tyr Met Gly Lys Val Leu
                       215
                                           220
Arg Leu Asn Leu Asp Gly Ser Ile Pro Lys Asp Asn Pro Ser Phe Asn
                   230
                                       235
Gly Val Val Ser His Ile Tyr Thr Leu Gly His Arg Asn Pro Gln Gly
                                  250
               2.45
Leu Ala Phe Thr Pro Asn Gly Lys Leu Leu Gln Ser Glu Gln Gly Pro
                               265
Asn Ser Asp Asp Glu Ile Asn Leu Ile Val Lys Gly Gly Asn Tyr Gly
                           280
Trp Pro Asn Val Ala Gly Tyr Lys Asp Asp Ser Gly Tyr Ala Tyr Ala
                       295
                                           300
Asn Tyr Ser Ala Ala Ala Asn Lys Ser Ile Lys Asp Leu Ala Gln Asn
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305

310

315

320

1500

1620

1680

1740

1776

1560

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Gly Val Lys Val Ala Ala Gly Val Pro Val Thr Lys Glu Ser Glu Trp
              325
                                330
Thr Gly Lys Asn Phe Val Pro Pro Leu Lys Thr Leu Tyr Thr Val Gln
                            345
Asp Thr Tyr Asn Tyr Asn Asp Pro Thr Cys Gly Glu Met Thr Tyr Ile
                        360
Cys Trp Pro Thr Val Ala Pro Ser Ser Ala Tyr Val Tyr Lys Gly Gly
                      375
Lys Lys Ala Ile Thr Gly Trp Glu Asn Thr Leu Leu Val Pro Ser Leu
                  390
                                     395
Lys Arg Gly Val Ile Phe Arg Ile Lys Leu Asp Pro Thr Tyr Ser Thr
              405
                                410
Thr Tyr Asp Asp Ala Val Pro Met Phe Lys Ser Asn Asn Arg Tyr Arg
                  425
Asp Val Ile Ala Ser Pro Asp Gly Asn Val Leu Tyr Val Leu Thr Asp
                        440
Thr Ala Gly Asn Val Gln Lys Asp Asp Gly Ser Val Thr Asn Thr Leu
                      455
Glu Asn Pro Gly Ser Leu Ile Lys Phe Thr Tyr Lys Ala Lys Glu Leu
                  470
                                     475
Gly Lys Ala Arg Met Pro Glu Phe Val Ala Gln Arg Thr Gly Gln Leu
              485
                                 490
Leu Gln Gly Val Lys Tyr Asp Pro Ala Lys Val Glu Ala Gly Thr Met
                  505
Leu Tyr Val Ala Asn Cys Val Phe Cys His Gly Val Pro Gly Val Asp
                         520
Arg Gly Gly Asn Ile Pro Asn Leu Gly Tyr Met Asp Ala Ser Tyr Ile
                      535
                                        540
Glu Asn Leu Pro Asn Phe Val Phe Lys Gly Pro Ala Met Val Arg Gly
                  550
                                     555
Met Pro Asp Phe Thr Gly Lys Leu Ser Gly Asp Asp Val Glu Ser Leu
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Lys Ala Phe Ile Gln Gly Thr Ala Asp Ala Ile Arg Pro Lys Pro
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29

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gggggagctc ggcaaggcca ggatgccgga
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<223> Description of Artificial Sequence: PCR primer
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ggggaagctt tcagggcttg ggccggatgg
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